

ABSTRACT OF THE DISCLOSURE

A method and interactive screen system for identifying orthologous genomic regions between two or more species can be provided. The method can involve performing a BLAST search using each of the two or more species against each of the other of the two or more species and identifying the best ortholog matches. The interactive screen system can display one or more of (a) a map viewer which can show genomic sequence information of the two or more species with markers therein, (b) a TA viewer which can show at least one contig and fragments which generated the contig, (c) an evidence viewer which can anotate transcribed regions of the genomic data, (d) a synteny viewer which can show syntenic relationships between the genomic sequence data, (e) a multiple sequence alignment viewer which can show multiple sequence alignments of genomic sequences, and (f) a trace viewer which can show single nucleotides in genomic sequences.